

Case 1-Commercial

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AUG 19 1999

U.S. GOVERNMENT PRINTING OFFICE: 1999 500-1000 18-JUN-1999
THE GREAT AMERICAN BOOK OF THE MONTHLY ALMANAC AND PREDICTION, 1999

REFERENCE
 AUTHOR: Padilayya, A.R., Lee, J.H. and Pei, J.J.
 TITLE: Identification of a general transcription factor TFIIAalpha/beta a homolog selectively expressed in testis
 JOURNAL: *J. Biol. Chem.* 274 (25), 18040-18048 (1999)
 MEDLINE
 ID: 99292779
 REFERENCE
 2 (bases 1 to 1617)
 AUTHOR: Padilayya, A.R. and Pei, J.J.
 TITLE: Direct Submission
 JOURNAL: *J. Biol. Chem.* 274 (25), 18040-18048 (1999)
 INSTITUTION: Molecular and Cell Biology, The University of Texas at Dallas, 2601 N. Floyd Rd., Richardson, TX 75080, USA
 FRACTION: Isolation, classifiers
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 CDS 16..1452
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 VSFGNHEHKINPEALLCHQESSHYISIPLGVVFSPQVSQTNSDVESVLSGSASMAQNLHD
 ESLSTSPPHGAHQVITDOLHILKNRPMYCCDSVKQPRNIHEPSNIPVSEKJCSNSQVDL
 SIRVTDDMIGEI1QVTDGSGQDTSSNEE1G51RCADENHFLGNTDQGDIKVPEEEAISIC
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Query Match: 100.0%; Score: 1617; DB: 39; Length: 1617;
 best local similarity: 100.0%; Freq. N: 17; Matches: 1617; Conservatism: 0; Mismatches: 0; Indels: 0; Gap: 0;

¹⁰ See, for example, the discussion of the 1992 Constitutional Convention in the *Constitutional Convention of 1992: The Final Report* (1993).

88 124. *Contaminants in the environment and their effects on health* (ed. J. M. Last, J. D. Wallace, and J. M. Vimpani), 1988.

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+>_xref="31:31668"
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YI LPPNSNCHI IAISSGESSI I FTRETFIIS HALLI SNGCTHPTI KVGI PIAFVNPQGA
HPLI FVLLMFLPFTGFFT PAGCIFKFLP VDLSHPTI PFIQSKMFSI PAKKMI IISI
KQMLKQSLNLYI CRRFLPHI QSAFNGDSIRSLSLNHGC LOAENASSFVPTI LFRSQQEKSGW
SPMLRIPFEKNNMMSI RIIWGLI PFLKVLFGTIIQMYIYEQGLEKPFKEIQLDIFYCRILSEEK
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VFFFPLMKLPANSKIFKNYEEQELI SLEI NDMFWGFTVKEDKFKVLSAVITQIYCLCFVNG
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AKRFELMLRFKTIYNNQDNLPSLSKQWNTVQGATVLEQAFUNMAI LAQRSSYAGSLRSCD
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ESAYQAVVWKIDRILFDKNSSLCTPHCISYFIALCSDQI PSCWYPFATVQFSI PDTCA
SRTEI RCLGVESI PVOQKHVQORACYNIQKLYFSVIEDNTI ECVRNLFASEGIEEDQVIL
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ENATSDI I LVS PGNEHKIVPEALI CHQFSSHYIISI PGVVPSQWSQTNSI VESVLSGSA
SMAQNLHDESLSI SFH GALHQHITD1QLH I LKNEHMTGCDSVKCPRNIEEPSNIPVSEK
DSNSQVDSLISRVTDIDIGI I QVGDGSGDTSSNEEIGSTRDADFNEFLGNIDGGDLFVP
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KTHRSKWKFKYLDGVMCFGGRDYVFAFAIGDAEW"

BASE COUNT 1149 a 302 c 811 g 1062 t
ORIGIN

Query Match 97.8%; Score 1582.2; IB 39; Length 3824;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1587; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

1080. CUSTODIA DE LOS DOCUMENTOS EN LOS ESTABLECIMIENTOS DE SALUD. 201

1400 *Journal of Performance Measurement* / Spring 2004 *Measuring and Managing Risk* 249

RESULT 3

AC023827/c

LOCUS AC023827 151767 bp DNA HTG 09-MAR-2000
DEFINITION Homo sapiens chromosome 16 clone RP11-4211B, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC023827
VERSION AC023827.2 GI:7711923
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151767)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL **Unpublished**
REFERENCE 2 (bases 1 to 151767)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted JSF-FFR-2000, Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 9, 2000 this sequence version replaced gi:6997147.

Center: Joint Genome Institute
Center Code: JGI
Web Address: <http://www.jgi.doe.gov>

Sequence quality: 100% clean, 0.0% bad, 0.0%
Instrument quality: 100% clean, 0.0% bad, 0.0%
Instrument quality: 100% clean, 0.0% bad, 0.0%
Estimated insert size: 151767; sum-of-squares estimation
Estimated insert size: 151767; unbiased-tp estimation
Quality coverage: 4.3x in Q20 bases; agarose-tp estimation
Quality coverage: 4.3x in Q20 bases; sum-of-squares estimation

* NGS: Next generation sequencing data; HTG: High-throughput sequencing data; HTGS: High-throughput sequencing data; JGI: Joint Genome Institute; JSF: Joint Sequencing Facility; FFR: Full genome resequencing.

PERMIT NO.

NUMBER 1000

DATE ISSUED: 04-FEB-1999

04-FEB-1999

REFERENCE Primates; Catarrhini; Hominidae; *Homo*.
AUTHORS 1 bases 1 to 1199
Honda,H.
TITLE *Primate classification*
SUBMITTED 01-APR-1991 to the DDBJ/EMBL/GenBank databases. Hiroshi
Honda, Tokyo Institute of Technology, Faculty of Bioscience and
Bio-technology; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa
227-8561, Japan (Tel:045-922-1111, Fax:045-923-0380)
REFERENCE 7 bases 1 to 1199
AUTHORS Watanabe,H., Oguri,K., Wada,T., Imai,T., Shiraya,T. and Honda,H.
TITLE Isolation of two cRNAs that encode the large subunit of human
transcription factor TFIIA
JOURNAL **Unpublished** (1993)
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AEW"
BASE COUNT 292 a 269 c 278 g 279 t
ORIGIN

Query Match 8.2 ; Score 132.4; PB 9; Length 1199;
Best Local Similarity 66.4 ; Previ. No. 1.3e-18;
Matches 191; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Table 3. Results of the first and second stage of the estimation of the model of the dynamics of the 1227

④ 《新民晚报》1949年1月10日。1949年1月10日，新民晚报社长王元化在《新民晚报》社长室，接待了由中共上海市委派来的代表，商讨《新民晚报》的改组问题。

RESULT : E
 HUMTFIIA48
 LOCUS HUMTFIIA48 1149 cp mRNA PRI 04-FEB-1999
 DEFINITION Human mRNA for TFIIA-42, complete cds.
 ACCESSION D14887
 VERSION D14387.1 GI:727196
 KEYWORDS TFIIA-42; transcription factor.
 SOURCE Homo sapiens cell_line:HeLa-S3 cDNA to mRNA, clone_lib:lambda gt10.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1549)
 AUTHORS Handa,H.
 TITLE Direct Submission.
 JOURNAL Submitted (05-APR-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
 Handa, Tokyo Institute of Technology, Faculty of Bioscience and
 Biotechnology; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa
 226-8501, Japan (Tel:045-922-1111, Fax:045-923-0380)
 2 (bases 355 to 1549)
 REFERENCE 2 (bases 355 to 1549)
 AUTHORS Watanabe,H., Oguri,K., Wada,T., Imai,T., Shiroya,T. and Handa,H.
 TITLE Isolation of two cDNAs that encode the large subunit of human
 transcription factor II A
 JOURNAL Unpublished (1993)
 FEATURES Location/Qualifiers
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 QQLQVVAANGAQYI FQPOQQSVLQQQVI PQMQPGGVQAFVIQQVLAPLPGI SPQQTG
 WITQPOQIILETGNKIQV1HTTVAAPTFQAOQTATGQQQFQACPAQTQAPLVLQVDST
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Query Match: 70.0%; Edit Distance: 10.0%; Gaps: 11.4%;
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